



OIEP

RAW SEQUENCE LISTING

DATE: 06/04/2002

PATENT APPLICATION: US/10/058,566

TIME: 12:20:39

Input Set : A:\Phi-1147.app

Output Set: N:\CRF3\06042002\J058566.raw

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3 <110> APPLICANT: ALBERTSEN, MARC
4   FOX, TIM
5   HUFFMAN, GARY
6   TRIMNELL, MARY
8 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
9   METHOD OF USING SAME
11 <130> FILE REFERENCE: PHI 1147
13 <140> CURRENT APPLICATION NUMBER: 10/058,566
14 <141> CURRENT FILING DATE: 2002-01-28
16 <160> NUMBER OF SEQ ID NOS: 8
18 <170> SOFTWARE: PatentIn Ver. 2.1
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22 <212> TYPE: DNA
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34 gtt gcc tct tgg ctt atc aaa cgg ctc ctc gag tct gga tat cat gtg 97
35   Val Ala Ser Trp Leu Ile Lys Arg Leu Leu Glu Ser Gly Tyr His Val
36     20           25           30
38 gta ggg act gtc agg gac cca gga aat cac caa aaa aca gcc cac ctt 145
39   Val Gly Thr Val Arg Asp Pro Gly Asn His Gln Lys Thr Ala His Leu
40     35           40           45
42 tgg aaa tta cct ggc gct aaa gag agg ctg caa atc gtg cga gct aat 193
43   Trp Lys Leu Pro Gly Ala Lys Glu Arg Leu Gln Ile Val Arg Ala Asn
44     50           55           60
46 ctg ttg gaa gaa ggg agc ttc gac agc gcc gtg atg gcc tgt gag ggt 241
47   Leu Leu Glu Glu Gly Ser Phe Asp Ser Ala Val Met Ala Cys Glu Gly
48     65           70           75           80
50 gta ttc cac act gca tcc ccc gtc ctc gct aaa ccc gac tct act agc 289
51   Val Phe His Thr Ala Ser Pro Val Leu Ala Lys Pro Asp Ser Thr Ser
52     85           90           95
54 aag gag gac acg ctc gtc cct gcg gtg aac ggt act ctg aac gtg ctg 337
55   Lys Glu Asp Thr Leu Val Pro Ala Val Asn Gly Thr Leu Asn Val Leu
56     100          105          110
58 aga tcg tgc aag aag aac ccc ttc ctg aaa agg gtc gtc ctt acg tct 385
59   Arg Ser Cys Lys Lys Asn Pro Phe Leu Lys Arg Val Val Leu Thr Ser
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62 tcg tcg tct gcg gtg agg atc agg gac gac ggt ggc cag tcc agt aac 433
63 Ser Ser Ser Ala Val Arg Ile Arg Asp Asp Gly Gly Gln Ser Ser Asn
64 130 135 140
66 atc tcg ctg gac gaa acg aca tgg agc tcc gtg cca ctc tgc gag aag 481
67 Ile Ser Leu Asp Glu Thr Thr Trp Ser Ser Val Pro Leu Cys Glu Lys
68 145 150 155 160
70 atg cat cta tgg tat gcc cta gcc aag gta ttt gca gag aaa gcg gcg 529
71 Met His Leu Trp Tyr Ala Leu Ala Lys Val Phe Ala Glu Lys Ala Ala
72 165 170 175
74 tgg gag ttc gcc aag gag aac ggc atc gac ctt gtg act gtc ctc ccg 577
75 Trp Glu Phe Ala Lys Glu Asn Gly Ile Asp Leu Val Thr Val Leu Pro
76 180 185 190
78 tcg ttc gtg atc ggg ccc agt ttg tcc cac gag cta tgc gtt acc gct 625
79 Ser Phe Val Ile Gly Pro Ser Leu Ser His Glu Leu Cys Val Thr Ala
80 195 200 205
82 tca gac gtc cta ggc cta ttc caa ggc gac acg gca agg ttc agc tcg 673
83 Ser Asp Val Leu Gly Leu Phe Gln Gly Asp Thr Ala Arg Phe Ser Ser
84 210 215 220
86 tac gga aga atg ggg tac gtc cac atc gac gac gtt gcg agc agc cac 721
87 Tyr Gly Arg Met Gly Tyr Val His Ile Asp Asp Val Ala Ser Ser His
88 225 230 235 240
90 atc ctg gtg tac gag gtc ccc cag gcc gcc ggg agg tac ctg tgc agc 769
91 Ile Leu Val Tyr Glu Val Pro Gln Ala Ala Gly Arg Tyr Leu Cys Ser
92 245 250 255
94 tca gtg gtg ctg gac aac gac gag ctg gtc tcc tcg ctc gcg aaa cgc 817
95 Ser Val Val Leu Asp Asn Asp Glu Leu Val Ser Ser Leu Ala Lys Arg
96 260 265 270
98 tac ccg ata ttc ccc ata ccc cgg agg ctg aac agc ccc tac ggc aag 865
99 Tyr Pro Ile Phe Pro Ile Pro Arg Arg Leu Asn Ser Pro Tyr Gly Lys
100 275 280 285
102 cag tcg tac cag ctg aac acg tcg aag ctg cag ggg ctg ggc ttc aag 913
103 Gln Ser Tyr Gln Leu Asn Thr Ser Lys Leu Gln Gly Leu Gly Phe Lys
104 290 295 300
106 ttc aga ggg gtg cag gag atg ttc gac gac tgc gtg cag tcg ctc aaa 961
107 Phe Arg Gly Val Gln Glu Met Phe Asp Asp Cys Val Gln Ser Leu Lys
108 305 310 315 320
110 gac cag gcc cac ctg ctg gag tgc ccc ctg tgaactgcga tgggggtgcc 1011
111 Asp Gln Gly His Leu Leu Glu Cys Pro Leu
112 325 330
114 tctctgtaac gcccggtttt ttttttttc aataattcca cgtcatgtca cgggtgtctc 1071
116 gcgcagactg ctactgtcag gtgtcagggc gtcatagtct acgggctcta cggctacatg 1131
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132 Val Ala Ser Trp Leu Ile Lys Arg Leu Leu Glu Ser Gly Tyr His Val
133      20      25      30
135 Val Gly Thr Val Arg Asp Pro Gly Asn His Gln Lys Thr Ala His Leu
136      35      40      45
138 Trp Lys Leu Pro Gly Ala Lys Glu Arg Leu Gln Ile Val Arg Ala Asn
139      50      55      60
141 Leu Leu Glu Glu Gly Ser Phe Asp Ser Ala Val Met Ala Cys Glu Gly
142      65      70      75      80
144 Val Phe His Thr Ala Ser Pro Val Leu Ala Lys Pro Asp Ser Thr Ser
145      85      90      95
147 Lys Glu Asp Thr Leu Val Pro Ala Val Asn Gly Thr Leu Asn Val Leu
148      100      105      110
150 Arg Ser Cys Lys Lys Asn Pro Phe Leu Lys Arg Val Val Leu Thr Ser
151      115      120      125
153 Ser Ser Ser Ala Val Arg Ile Arg Asp Asp Gly Gly Gln Ser Ser Asn
154      130      135      140
156 Ile Ser Leu Asp Glu Thr Thr Trp Ser Ser Val Pro Leu Cys Glu Lys
157      145      150      155      160
159 Met His Leu Trp Tyr Ala Leu Ala Lys Val Phe Ala Glu Lys Ala Ala
160      165      170      175
162 Trp Glu Phe Ala Lys Glu Asn Gly Ile Asp Leu Val Thr Val Leu Pro
163      180      185      190
165 Ser Phe Val Ile Gly Pro Ser Leu Ser His Glu Leu Cys Val Thr Ala
166      195      200      205
168 Ser Asp Val Leu Gly Leu Phe Gln Gly Asp Thr Ala Arg Phe Ser Ser
169      210      215      220
171 Tyr Gly Arg Met Gly Tyr Val His Ile Asp Asp Val Ala Ser Ser His
172      225      230      235      240
174 Ile Leu Val Tyr Glu Val Pro Gln Ala Ala Gly Arg Tyr Leu Cys Ser
175      245      250      255
177 Ser Val Val Leu Asp Asn Asp Glu Leu Val Ser Ser Leu Ala Lys Arg
178      260      265      270
180 Tyr Pro Ile Phe Pro Ile Pro Arg Arg Leu Asn Ser Pro Tyr Gly Lys
181      275      280      285
183 Gln Ser Tyr Gln Leu Asn Thr Ser Lys Leu Gln Gly Leu Gly Phe Lys
184      290      295      300
186 Phe Arg Gly Val Gln Glu Met Phe Asp Asp Cys Val Gln Ser Leu Lys
187      305      310      315      320
189 Asp Gln Gly His Leu Leu Glu Cys Pro Leu
190      325      330
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194 <211> LENGTH: 2544
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196 <213> ORGANISM: Zea mays
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200 ctctgcaatc cgtgcctgtg aagcaaatgg cgcagtcgcc tacttatcac accaacttat 120
201 cacctagaaa agcgacgcgt cctggatcga ttgcaaatct acctccaacc aaccagctt 180

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202 tgtatctgct tactgtgac accaaagtgt tgctgatacg atgtgcgatt attgctcttt 240
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204 ccagtgctcta gctgagaaca tggtagacct aagcaagggc aaggtatgcy taaccggggc 360
205 ctacaggcttt gtgcctcttt gtgcctcttt ggcctatcaa accgctcttc gactctggat atcatgtgt 420
206 agggactgtc agggaccagc gtatttgca aatatcatta ctatcgatc atctctcttt 480
207 attacattaa taattcttga ttaccaattt ttctttttt ttttttgta accacaagg 540
208 aataaccaaa aagacagccc acctttggaa attacctggc gctaaagaga ggctgcaaat 600
209 cgtgcgagct gatctgttgg aagaaggagg ctctgacagc gccgtgatgc cctgtgagg 660
210 tgtattccac actgcatccc ccgtcctcgc taaacccgac tctactgaca aggcattgca 720
211 tcgccgata tatatatgca tatctggacc atgcatccta ctgacgact ctgatacgg 780
212 aagcgcgttg catctaccgt acgtgaagct gcggtgaacg gtactctgaa cgtgctgaga 840
213 tgcattgtgc agggagacac gctgctccct gtcttcttta cgtcttcgct gtctgcggtg 900
214 tcgtgcaaga agaaccgctt ccgtaaacagg cctgcaaaag gacatggagc 960
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234 ctgcaactt ccgttctgct tgtgtactgt tggctgccc cgtatcaacc aacgcatgt 2160
235 ctgatgatgt tgatcggagg caggcacccg tgcattcagc tcatcgagat ttgcaaccg 2220
236 ggcgttttgg atggacgaat ggctccacca agattcagtc tcaaatccca aattctcga 2280
237 tgaattgttc cactggagcc actagcatca agattcagtc tcaaatccca aattctcga 2340
238 cgaagaagcca caaagagaga atgaatgtac agtgtttcaa gccacagctc actagctcaa 2400
239 aagtagtgag catgcacacc atgaatgtac agtgtttcaa gccacagctc actagctcaa 2460
240 ttgtacactt tgtataccaa ccaaccaacc aaccaagcaa gcaatcaagc aaacacagag 2520
241 agcaaacctg acgtggctgg cgcc
244 <210> SEQ ID NO: 4
246 <400> SEQUENCE: 4
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251 <211> LENGTH: 322
252 <212> TYPE: DNA
253 <213> ORGANISM: Zea mays
255 <400> SEQUENCE: 5
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259 tgtatctgct tactgtgatc accaaagttg tgctgatacg atgtgcgatt attgctcttt 240
260 cttctctaga atgttcttgc cgaatgctta taagagaagg ttggtcagca tcgatctctg 300
261 ccagtgctta gctgagaaca tg
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265 <211> LENGTH: 187
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267 <213> ORGANISM: Zea mays
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271 tgatcaccaa agttgtgctg atacgatgtg cgattattgc tctttctct ctagaatgtt 120
272 cctgccgatg ctttataaga gaaggttggt cagcatcgat ctctgccagt gctagactga 180
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277 <211> LENGTH: 697
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279 <213> ORGANISM: Sorghum sp.
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283 <222> LOCATION: (1)..(696)
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288 1 5 10 15
290 ctc gag tct gga tat cat gtg gta ggg act gtc aga gac cca gga aat 96
291 Leu Glu Ser Gly Tyr His Val Val Gly Thr Val Arg Asp Pro Gly Asn
292 20 25 30
294 cac caa aaa aca gca cac ctt tgg aaa tta cct ggt gcc aaa gag agg 144
295 His Gln Lys Thr Ala His Leu Trp Lys Leu Pro Gly Ala Lys Glu Arg
296 35 40 45
298 ctg caa att gtg cga gct gat ctg ttg gaa gaa ggg agc ttt gac aat 192
299 Leu Gln Ile Val Arg Ala Asp Leu Leu Glu Glu Gly Ser Phe Asp Asn
300 50 55 60
302 gct gtc atg gac tgt gat ggc gtc ttc cac act gca tcc cct gtg ctc 240
303 Ala Val Met Asp Cys Asp Gly Val Phe His Thr Ala Ser Pro Val Leu
304 65 70 75
306 gct aaa tct gat tct agt agc aag gag gaa acg ctt tgt cca gca gta 288
307 Ala Lys Ser Asp Ser Ser Ser Lys Glu Glu Thr Leu Cys Pro Ala Val
308 85 90 95
310 aac ggt act ctg aat gtg cta aga tgc tgc aag aag aac cca ttt ctg 336
311 Asn Gly Thr Leu Asn Val Leu Arg Ser Cys Lys Lys Asn Pro Phe Leu
312 100 105 110
314 aaa agg gtt gtt ctt acg tct tca tca tct gca gtg agg att agg gat 384
315 Lys Arg Val Val Leu Thr Ser Ser Ser Ser Ala Val Arg Ile Arg Asp
316 115 120 125
318 gat gat cag cct aat atc tca ctg gat gaa aca aca tgg agc tct gtg 432
319 Asp Asp Gln Pro Asn Ile Ser Leu Asp Glu Thr Thr Trp Ser Ser Val
320 130 135 140

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VERIFICATION SUMMARY

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Input Set : A:\Phi-1147.app

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